



09/869,414
Cstc 4
1/2
MAY 04 2005
I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail, in an envelope addressed to: MS Post Issue, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on the date shown below.

Dated: May 2, 2005

Signature: *Jeanne Brashear*
(Jeanne M. Brashear)

Docket No.: 29915/6280MUS
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Letters Patent of:
Mark E. Gurney et al.

Patent No.: 6,790,610

Issued: September 14, 2004

For: ALZHEIMER'S DISEASE, SECRETASE, APP
SUBSTRATES THEREFOR, AND USES
THEREFOR

**Certificate
MAY 11 2005
of Correction**

REQUEST FOR CERTIFICATE OF CORRECTION PURSUANT TO 37 CFR 1.323

MS Post Issue
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

Patentees respectfully request a Certificate of Correction to be issued for the above-identified U.S. Patent correcting the patent as noted in the attached "Certificate of Correction" form PTO/SB/144. Duplicate copies of the form are attached hereto.

At column 9, lines 63-64 please delete "according to claim 14 or a vector according to claim 15 or 16" and insert --of the invention or a vector of the invention-- immediately following "polynucleotide". This correction is intended to omit references to particular claims and to add general language to make these statements clear and concise. This correction was approved by the Certificate of Correction Branch of the United States Patent and Trademark Office in parent application serial no. 09/416,901, now U.S. Patent No. 6,699,671. This correction does not add new matter to the patent.

05/05/2005 AKELECH2 00000036 6790610

01 FC:1811

100.00 OP

MAY 12 2005

Errors in the patent can be verified by reference to the application as follows:

<u>Appln. Page #</u>	<u>Appln. Line #</u>	<u>Column #</u>	<u>Line #</u>	<u>Error By</u>
1	1	Cover page Section (54)	1	PTO
Terminal disclaimer 3/21/04	--	Cover page Section (*)	--	PTO
PTO/Form/892	--	Cover page 2 Column 1	5	PTO
1	1	1	1	PTO
2	20	2	3	PTO
5	14	3	56	Applicant
6	9	4	24	Applicant
7	16	5	10	Applicant
8	14	5	49	Applicant
9	17	6	28	Applicant
12	12	8	6	PTO
Amendment Dated 05/27/03	Page 2	8	16	Applicant
13	4	8	37	Applicant
13	24	8	64	Applicant
13	28	9	3	Applicant
14	22	9	38	Applicant
14	24	9	40	Applicant
15	1	9	51	Applicant
15	21	10	12	Applicant
17	24	11	37	Applicant

<u>Appln. Page #</u>	<u>Appln. Line #</u>	<u>Column #</u>	<u>Line #</u>	<u>Error By</u> Applicant
18	5	11	53	
24	23	16	11	Applicant
25	19	16	48	PTO
26	2	16	65	PTO
26	29	17	37	PTO
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Amendment Dated 5/27/03	page 3, line 9	21	12	PTO
39	9	25	12	Applicant
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52	2	33	8	Applicant
53	10	33	60	PTO
53	12	33	63	Applicant
53	15	33	66	PTO
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59	17	36	63	Applicant
64	8	39	17	PTO
64	9	39	18	PTO
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64	14	39	26	PTO
66	24	40	51	Applicant

<u>Appln. Page #</u>	<u>Appln. Line #</u>	<u>Column #</u>	<u>Line #</u>	<u>Error By</u>
67	5	40	67	PTO
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67	10	41	5	PTO
67	19	41	17	Applicant
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75	8	45	37	PTO
75	12	45	43	PTO
75	27	45	65	Applicant
77	15	46	65	Applicant
79	9	48	1	PTO
76	16	48	11	PTO
81	6	49	16	PTO
Amendment Dated 1/5/04	Sequence Listing pages 1-63	Sequence listing Columns 49-164		PTO
Examiner's Amendment Claim 155, lines 3-4		163 claim 1	43-44	PTO
Examiner's Amendment Claim 155, lines 8-10		163 claim 1	51-54	PTO
Examiner's Amendment Claim 162, line 1		164 claim 6	45	PTO
Examiner's Amendment Claim 164, line 1		164 claim 8	50	PTO
Examiner's Amendment Claim 166, line 1		164 claim 10	56	PTO

At least one of the errors were found in the application as filed by applicant.
Our check in the amount of \$100.00 covering the fee set forth in 37 CFR 1.20(a) is enclosed.

The errors now sought to be corrected are inadvertent typographical errors the correction of which does not involve new matter or require reexamination.

Transmitted herewith is a proposed Certificate of Correction effecting such amendment. Patentee respectfully solicits the granting of the requested Certificate of Correction.

The Director is hereby authorized to charge any deficiency in the fees filed, asserted to be filed or which should have been filed herewith (or with any paper hereafter filed in this application by this firm) to our Deposit Account No. 13-2855, under Order No. 29915/6280MUS. A duplicate copy of this paper is enclosed.

Dated: May 2, 2005

Respectfully submitted,

By Jeanne Brashear
Jeanne M. Brashear
Registration No.: 56,301
MARSHALL, GERSTEIN & BORUN LLP
233 S. Wacker Drive, Suite 6300
Sears Tower
Chicago, Illinois 60606-6357
(312) 474-6300
Agent for Applicant

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,790,610

DATED : September 14, 2004

INVENTOR(S) : Mark E. Gurney et al.

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Cover Sheet:

At Section 54, column 1, please delete "Disease, Secretase" and insert --Disease Secretase--.

At Section (*), column 1, please insert --This patent is subject to a terminal disclaimer--.

On page 2, column 1, line 5, please delete "th" and insert --the--.

In the Specification:

At Column 1, line 1, please delete "Disease, Secretase" and insert --Disease Secretase--.

At Column 2, line 3, please delete "a-site" and insert --a site--.

At Column 3, line 56, please insert --of-- before "those".

At Column 4, line 24, please delete "lease" and insert --least--.

At Column 5, line 10, please insert --to-- before "any".

At Column 5, line 49, please insert --of-- before "those".

At Column 6, line 28, please delete "lease" and insert --least--.

At Column 8, line 6, please insert --iii) select the cells which produce the critical peptide-- after "APP".

At Column 8, line 16, please insert --(SEQ ID NO: 74)-- after "P2".

At Column 8, line 37, please delete "has" and insert --as--.

At Column 8, line 64, please delete "Measurment" and insert --Measurement--.

At Column 9, line 3, please delete "reporter-protein" and insert --reporter protein--.

At Column 9, line 38, please delete "construct" and insert --constructed--.

At Column 9, line 40, please delete "streiches" and insert --stretches--.

At Column 9, line 51, please delete "recombinant" and insert --recombinant--.

At Column 10, line 12, please delete "hyrdrophobic" and insert --hydrophobic--.

MAILING ADDRESS OF SENDER:

Jeanne M. Brashear

MARSHALL, GERSTEIN & BORUN LLP

233 S. Wacker Drive, Suite 6300

Sears Tower

Chicago, Illinois 60606-6357

PATENT NO. 6,790,610

No. of additional copies

MAY 12 2005

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In the Specification, (cont'd):

At Column 11, line 37, please delete "oassays" and insert --bioassays--.
 At Column 11, line 53, please delete "on" and insert --one--.
 At Column 16, line 11, please delete "Fig. 11" and insert --Fig. 12--.
 At Column 16, line 48, please delete "I)" and insert --ID--.
 At Column 16, line 65, please delete "Glutarnine" and insert --Glutamine--.
 At Column 17, line 37, please delete "α-secretase" and insert --β-secretase--.
 At Column 18, line 38, please delete "possible" and insert --possibly--.
 At Column 21, line 12, please delete "6" and insert --6--.
 At Column 25, line 12, please delete "embyonic" and --embryonic--.
 At column 30, line 28, please delete "Hu-ASPI" and insert --Hu-asp1--.
 At column 31, line 20, please delete "sequence" and insert --sequenced--.
 At column 32, line 42, please insert --to-- before "contain".
 At column 33, line 8, please delete "manufacture" and insert --manufacturer--.
 At column 33, line 60, please delete "Phospho1mager" and insert --PhosphorImager--.
 At column 33, line 63, please delete "is" and insert --in--.
 At column 33, line 66, please delete "CDNA" and insert --cDNA--.
 At column 35, line 59, please delete "AP" and insert --Aβ--.
 At column 36, line 63, please delete "prority" and insert --proprietary--.
 At column 39, line 17, please delete "AP" and insert --Aβ--.
 At column 39, line 18, please delete "AP" and insert --Aβ--.
 At column 39, line 24, please delete "AP" and insert --Aβ--.
 At column 39, line 26, please delete "P42" and insert --β42--.
 At column 39, line 26, please delete "γ-secretase" and insert --γ-secretase--.
 At column 40, line 51, please delete "Ab" and insert --Aβ--.
 At column 40, line 67, please delete "βP40" and insert --Aβ40--.
 At column 40, line 67, please delete "βP42" and insert --Aβ42--.
 At column 41, line 5, please delete "βP42" and insert --Aβ42--.
 At column 41, line 17, please delete "Ab." and insert --Aβ--.
 At column 44, line 50, please delete "internediate" and insert --intermediate--.
 At column 45, line 37, please delete "2O" and insert --20--.

MAILING ADDRESS OF SENDER:

Jeanne M. Brashear
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 Sears Tower
 Chicago, Illinois 60606-6357

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At column 45, line 43, please delete "101 M" and insert --101 μ M--.
At column 45, line 65, please delete "Hu-ASp2(b)" and insert --Hu-Asp2(b)--.
At column 46, line 65, please delete "prepared" and insert --prepare--.
At column 48, line 1, please delete "(1/250)" and insert --(1/2500)--.
At column 48, line 11, please delete "K1" and insert --K1--.
At column 49, line 16, please delete "Swedigh" and insert --Swedish--.

In the Sequence Listing:

Please delete the sequence listing as published and replace with the paper copy attached hereto.

In the Claims:

In claim 1, at column 163, lines 43-44, please delete "FIG. 3 (SEQ ID NO: 4)," and insert --FIG. 4, (SEQ ID NO: 3),--.

In claim 1, at column 163, lines 51-54, please delete ", and wherein the polypeptide exhibits aspartyl protease activity involved in processing APP into amyloid beta." and insert ---.

In claim 6, at column 164, line 45, please delete "A host" and insert --An isolated host--.

In claim 8, at column 164, line 50, please delete "derived from" and insert -- that is--.

In claim 10, at column 164, line 56, please delete "A host" and insert --An isolated host--.

MAILING ADDRESS OF SENDER:

Sharon M. Sintich
MARSHALL, GERSTEIN & BORUN LLP
233 S. Wacker Drive, Suite 6300
Sears Tower
Chicago, Illinois 60606-6357

PATENT NO. 6,790,610

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22313-1450, on the date shown below.

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2	20	2	3	PTO
5	14	3	56	Applicant
6	9	4	24	Applicant
7	16	5	10	Applicant
8	14	5	49	Applicant
9	17	6	28	Applicant
12	12	8	6	PTO
Amendment Dated 05/27/03	Page 2	8	16	Applicant
13	4	8	37	Applicant
13	24	8	64	Applicant
13	28	9	3	Applicant
14	22	9	38	Applicant
14	24	9	40	Applicant
15	1	9	51	Applicant
15	21	10	12	Applicant
17	24	11	37	Applicant

<u>Appln. Page #</u>	<u>Appln. Line #</u>	<u>Column #</u>	<u>Line #</u>	<u>Error By</u>
		11	53	Applicant
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24	23	16	11	Applicant
25	19	16	48	PTO
26	2	16	65	PTO
26	29	17	37	PTO
28	17	18	38	Applicant
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47	21	30	28	PTO
49	5	31	20	Applicant
51	8	32	42	Applicant
52	2	33	8	Applicant
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66	24	40	51	Applicant

<u>Appln. Page #</u>	<u>Appln. Line #</u>	<u>Column #</u>	<u>Line #</u>	<u>Error By</u>
67	5	40	67	PTO
67	6	40	67	PTO
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67	19	41	17	Applicant
73	23	44	50	PTO
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75	12	45	43	PTO
75	27	45	65	Applicant
77	15	46	65	Applicant
79	9	48	1	PTO
76	16	48	11	PTO
81	6	49	16	PTO
Amendment Dated 1/5/04	Sequence Listing pages 1-63	Sequence listing Columns 49-164		PTO
Examiner's Amendment Claim 155, lines 3-4		163 claim 1	43-44	PTO
Examiner's Amendment Claim 155, lines 8-10		163 claim 1	51-54	PTO
Examiner's Amendment Claim 162, line 1		164 claim 6	45	PTO
Examiner's Amendment Claim 164, line 1		164 claim 8	50	PTO
Examiner's Amendment Claim 166, line 1		164 claim 10	56	PTO

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Dated: May 2, 2005

Respectfully submitted,

By Jeannie Brashear
Jeannie M. Brashear

Registration No.: 56,301
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233 S. Wacker Drive, Suite 6300
Sears Tower
Chicago, Illinois 60606-6357
(312) 474-6300
Agent for Applicant

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,790,610

DATED : September 14, 2004

INVENTOR(S) : Mark E. Gurney et al.

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 At Column 2, line 3, please delete "a-site" and insert --a site--.
 At Column 3, line 56, please insert --of-- before "those".
 At Column 4, line 24, please delete "lease" and insert --least--.
 At Column 5, line 10, please insert --to-- before "any".
 At Column 5, line 49, please insert --of-- before "those".
 At Column 6, line 28, please delete "lease" and insert --least--.
 At Column 8, line 6, please insert --iii) select the cells which produce the critical peptide.-- after "APP".
 At Column 8, line 16, please insert --(SEQ ID NO: 74)-- after "P2".
 At Column 8, line 37, please delete "has" and insert --as--.
 At Column 8, line 64, please delete "Measurment" and insert --Measurement--.
 At Column 9, line 3, please delete "reporter-protein" and insert --reporter protein--.
 At Column 9, line 38, please delete "construct" and insert --constructed--.
 At Column 9, line 40, please delete "streiches" and insert --stretches--.
 At Column 9, line 51, please delete "recombinant" and insert --recombinant--.
 At Column 10, line 12, please delete "hydophobic" and insert --hydrophobic--.

MAILING ADDRESS OF SENDER:

Jeanne M. Brashear
 MARSHALL, GERSTEIN & BORUN LLP
 233 S. Wacker Drive, Suite 6300
 Sears Tower
 Chicago, Illinois 60606-6357

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At column 36, line 63, please delete "proprietary" and insert --proprietary--.
At column 39, line 17, please delete "AP" and insert --Aβ--.
At column 39, line 18, please delete "AP" and insert --Aβ--.
At column 39, line 24, please delete "AP" and insert --Aβ--.
At column 39, line 26, please delete "P42" and insert --β42--.
At column 39, line 26, please delete "y-secretase" and insert --y-secretase--.
At column 40, line 51, please delete "Ab" and insert --Aβ--.
At column 40, line 67, please delete "βP40" and insert --Aβ40--.
At column 40, line 67, please delete "βP42" and insert --Aβ42--.
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At column 45, line 37, please delete "2O" and insert --20--.

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At column 45, line 65, please delete "Hu-Asp2(b)" and insert --Hu-Asp2(b)--.

At column 46, line 65, please delete "prepared" and insert --prepare--.

At column 48, line 1, please delete "(1/250)" and insert --(1/2500)--.

At column 48, line 11, please delete "KI" and insert --K1--.

At column 49, line 16, please delete "Swedigh" and insert --Swedish--.

In the Sequence Listing:

Please delete the sequence listing as published and replace with the paper copy attached hereto.

In the Claims:

In claim 1, at column 163, lines 43-44, please delete "FIG. 3 (SEQ ID NO: 4)," and insert --FIG. 4, (SEQ ID NO: 3)--.

In claim 1, at column 163, lines 51-54, please delete ", and wherein the polypeptide exhibits aspartyl protease activity involved in processing APP into amyloid beta." and insert ----.

In claim 6, at column 164, line 45, please delete "A host" and insert --An isolated host--.

In claim 8, at column 164, line 50, please delete "derived from" and insert -- that is--.

In claim 10, at column 164, line 56, please delete "A host" and insert --An isolated host--.

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Sharon M. Sintich
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- 1 -

SEQUENCE LISTING

<110> Gurney et al.

<120> ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR

<130> 28341/6280M

<140> US 09/869,414

<141> 2001-06-27

<150> US 09/416,901

<151> 1999-10-13

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<151> 1999-09-23

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<151> 1999-09-23

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gchgctgcgcc tggagcctgc cttggcgtcc cccgcggggcg cccgcaactt cttggccatg 240
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<212> PRT
<213> Homo sapiens

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35 40 45
Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
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Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65 70 75 80
Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
85 90 95
Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100 105 110
Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
115 120 125
Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
130 135 140
Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145 150 155 160
Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
165 170 175
Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
180 185 190
Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
195 200 205
Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
210 215 220
Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225 230 235 240
Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
245 250 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
260 265 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
275 280 285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
290 295 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305 310 315 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
355 360 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
370 375 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
450 455 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
485 490 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
500 505 510

Val Arg His Arg Trp Lys
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<210> 3
<211> 2070
<212> DNA
<213> Homo sapiens

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ataaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa

2070

<210> 4
<211> 501
<212> PRT
<213> Homo sapiens

<400> 4

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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln

210

215

220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
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<210> 5
<211> 1977
<212> DNA
<213> Homo sapiens

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1977

<210> 6
<211> 476
<212> PRT
<213> Homo sapiens

<400> 6

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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser

20

25

30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
420 425 430

Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
435 440 445

Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
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His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
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<210> 7

<211> 2043

<212> DNA

<213> Mus musculus

<400> 7

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gaa 2043

<210> 8
<211> 501
<212> PRT
<213> Mus musculus

<400> 8
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Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
195 200 205

Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val

275	280	285
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290	295	300
Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp		
305	310	315
Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr		
325	330	335
Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val		
340	345	350
Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg		
355	360	365
Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala		
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Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu		
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Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala		
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Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu		
420	425	430
Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro		
435	440	445
Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala		
450	455	460
Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp		
465	470	475
Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp		
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Ile Ser Leu Leu Lys		
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<212> DNA
<213> Homo sapiens
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35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
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His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
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Phe Phe Glu Gln Met Gln Asn
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<212> DNA

<213> Homo sapiens

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35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr

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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn		
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560		
Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr		
565	570	575
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser		
580	585	590
Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val		
595	600	605
His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys		
610	615	620
Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val		
625	630	635
640		
Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile		
645	650	655
His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg		
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His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys		
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35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
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Phe Phe Glu Gln Met Gln Asn
690 695

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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
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Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
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Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
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Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
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Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala
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Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
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His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
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35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
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Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
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Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
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Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
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Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
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Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
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Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
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 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
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Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
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Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
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Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
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Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
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Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
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Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
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Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
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Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
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Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
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Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
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Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
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Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
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Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
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Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
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Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
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Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
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Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
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Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
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Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val

595

600

605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
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Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
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Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
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His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
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His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
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<212> DNA

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acggcagcgg tggaaaggccc tttgtcacc ttggacatgg aagactgtgg ctacaacatt 1320
ccacagacag atgagtcatg a 1341

<210> 22

<211> 446

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln
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His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu

20	25	30
Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly		
35	40	45
Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser		
50	55	60
Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr		
65	70	75
Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala		
85	90	95
Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser		
100	105	110
Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly		
115	120	125
Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly		
130	135	140
Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp		
145	150	155
160		
Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala		
165	170	175
Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Asp		
180	185	190
Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu		
195	200	205
Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val		
210	215	220
Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly		
225	230	235
240		
Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile		
245	250	255
Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys		
260	265	270
Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu		
275	280	285
Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala		
290	295	300
Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln		
305	310	315
320		
Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val		
325	330	335
Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile		
340	345	350

Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr
355 360 365

Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly
370 375 380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp
385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
435 440 445

<210> 23

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 23

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ggggggccccc ccctggggct gcggctgccc cgggagaccg acgaagagcc cgaggagccc 180
ggccggaggg gcagctttgt ggagatgggtg gacaacctga ggggcaagtc ggggcagggc 240
tactacgtgg agatgaccgt gggcagccccc cgcagacgc tcaacatctt ggtggataca 300
ggcagcagta actttgcagt ggggtgctgcc ccccacccct tcctgcacg ctactaccag 360
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aactgggaag gcatctctggg gctggcctat gctgagattt ccaggcctga cgactccctg 600
gagcctttt ttgactctctt ggtaaaggcag acccacgttc ccaaccttctt ctcctgcac 660
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<210> 24

<211> 459

<212> PRT

<213> Homo sapiens

<400> 24

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15

Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
20 25 30

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg

35	40	45
Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly		
50	55	60
Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly		
65	70	75
80		
Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile		
85	90	95
Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His		
100	105	110
Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg		
115	120	125
Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu		
130	135	140
Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val		
145	150	155
160		
Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe		
165	170	175
Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu		
180	185	190
Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val		
195	200	205
Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala		
210	215	220
Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser		
225	230	235
240		
Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp		
245	250	255
Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg		
260	265	270
Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn		
275	280	285
Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro		
290	295	300
Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser		
305	310	315
320		
Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys		
325	330	335
Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu		
340	345	350
Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu		
355	360	365

Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
370 375 380

Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
385 390 395 400

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
405 410 415

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
420 425 430

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
435 440 445

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
450 455

<210> 25

<211> 1302

<212> DNA

<213> Homo sapiens

<400> 25

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gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180
gtgggcagcc ccccgagac gctcaacatc ctgggtgata caggcagcag taactttgca 240
gtgggtgctg ccccccaccc cttctgtcat cgctactacc agaggcagct gtccagcaca 300
taccgggacc tccggaaggg tggatgtt ccctacaccc agggcaagtg ggaaggggag 360
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gctgccatca ctgaatcaga caagttctc atcaacggct ccaactggga aggcatcctg 480
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gaccactcgc tgcacacagg cagtctctgg tatacaccca tccggcggga gtggatttat 720
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tacaactatc acaagagcat tggatgtt ggcacccatc accttcgttt gcccaagaaa 840
gtgtttgaag ctgcagtcaa atccatcaag gcagccctc ccacggagaa gttccctgat 900
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catgtgcacg atgagttcag gacggcagcg gtggaaaggcc cttttgtcac cttggacatg 1260
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<210> 26

<211> 433

<212> PRT

<213> Homo sapiens

<400> 26

Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly
1 5 10 15

Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu
20 25 30

Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
35 40 45

Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
50 55 60

Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
65 70 75 80

Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln
85 90 95

Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
100 105 110

Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
115 120 125

Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
130 135 140

Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
145 150 155 160

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro
165 170 175

Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
180 185 190

Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
195 200 205

Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
210 215 220

Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
225 230 235 240

Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
245 250 255

Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
260 265 270

Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
275 280 285

Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
290 295 300

Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
305 310 315 320

Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
325 330 335

Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
340 345 350

Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
355 360 365

Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
370 375 380

Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
385 390 395 400

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val
405 410 415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
420 425 430

Ser

<210> 27

<211> 1278

<212> DNA

<213> Homo sapiens

<400> 27

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ggcaagtccgg ggcaggggcta ctacgtggag atgaccgtgg gcagcccccc gcagacgctc 180
aacatcctgg tggatcacagg cagcagtaat tttcgtggat gtgctggccc ccaccccttc 240
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tatgtgcctt acacccaggg caagtgggaa ggggagctgg gcaccgcacct ggttaagcatc 360
ccccatggcc ccaacgtcac tgcgtgtcc aacattgtctt ccatcaactga atcagacaag 420
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aggcctgacg actccctggaa gcctttcttt gactctctgg taaaggcagac ccacgttccc 540
aacctcttctt ccctgcaccc ttgtgggtgtt ggctccccc tcaaccagtc tgaagtgtc 600
gcctctgtcg gagggagcat gatcattggaa ggtatcgacc actcgctgtt cacaggcagt 660
ctctggatata caccatccg gcgggagttgg tattatgagg tcatcattgtt gcccgtggag 720
atcaatggac aggatctgaa aatggactgc aaggagtaca actatgacaa gagcattgtg 780
gacagtggca ccaccaaccc tcgtttgtcc aagaaaagtgtt ttgaagctgc agtcaaatcc 840
atcaaggcag cctcctccac ggagaagttt cctgtatgggt tctggcttgg agagcagctg 900
gtgtgtggc aagcaggcac cacccttgg aacatttcc cagtcatctc actctaccta 960
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gcagcgggtgg aaggcccttt tgtcacccctt gacatggaaactgtggcta caacattcca 1260
cagacagatg agtcatga 1278

<210> 28

<211> 425

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15

Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe
20 25 30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr
35 40 45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
50 55 60

Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe
65 70 75 80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
85 90 95

Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
100 105 110

Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
115 120 125

Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn
130 135 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala
145 150 155 160

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln
165 170 175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe
180 185 190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile
195 200 205

Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr
210 215 220

Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu
225 230 235 240

Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp
245 250 255

Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys
260 265 270

Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu
275 280 285

Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln
290 295 300

Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu
305 310 315 320

Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln
325 330 335

Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys
340 345 350

Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala
355 360 365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg
370 375 380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr
385 390 395 400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly
405 410 415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425

<210> 29
<211> 1362
<212> DNA
<213> Homo sapiens

<400> 29
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ctgcggctgc cccggagac cgacgaagag cccgaggagc cggccggag gggcagctt 180
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gaagactgtg gtcacacat tccacagaca gatgagtcat ga 1362

<210> 30
<211> 453
<212> PRT
<213> Homo sapiens

<400> 30
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60 80

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser
450

<210> 31
<211> 1380
<212> DNA
<213> Homo sapiens

<400> 31
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ctgcggctgc cccggagac cgacgaagag cccgaggagc cccggccggag gggcagctt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
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taccgggacc tccggaaggg tggatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctgggcaccc acctgtaag catccccat gcccccaacg tcactgtgcg tgccaaacatt 480
gctgcccata ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg 540
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccctt cttgactct 600
ctggtaaaggc agaccacagt tcccaaccc tcctccctgc acctttgtgg tgctggcttc 660
cccccataacc agtctgaagt gctggccctt gtggaggga gcatgatcat tggaggtatc 720
gaccactcg tgcacacagg cagtctctgg tatacaccca tccggcggga gtggattat 780
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
tacaactatg acaagagcat tgggacactt ggcacccatc accttcgtt gccaagaaaa 900
gtgtttgaag ctgcagtcaa atccatcaag gcagccctt ccacggagaa gttccctgat 960
ggttctggc taggagagca gctgggtgtc tggcaaggag ccaccacccc ttggaacatt 1020
ttccccatca tctcactcta ctaatgggt gagttacca accagtccctt ccgcatcacc 1080
atccttccgc agcaataacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
tacaagttt ccacatcaca gtcatccacg ggcactgtt tggagctgt tattatggag 1200
ggcttctacg ttgtcttga tcggggccca aaacaattt gctttgtgt cagcgcttgc 1260
catgtgcacg atgagttcag gacggcagcg gtggaaaggcc ctttgcac cttggacatg 1320
gaagactgtg gctacaacat tccacagaca gatgagtac agcagcagca gcagcagtga 1380

<210> 32
<211> 459
<212> PRT
<213> Homo sapiens

<400> 32
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60 80

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser His His His His His His His
450 455

<210> 33
<211> 25
<212> PRT
<213> Homo sapiens

<400> 33
Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu
1 5 10 15
Ser Ser Leu Val Arg His Arg Trp Lys
20 25

<210> 34
<211> 19
<212> PRT
<213> Homo sapiens

<400> 34
Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
1 5 10 15
Leu Leu Lys

<210> 35
<211> 29
<212> DNA
<213> Homo sapiens

<400> 35
gtggatccac ccagcacggc atccggctg

29

<210> 36
<211> 36
<212> DNA
<213> Homo sapiens

<400> 36
gaaagcttc atgactcatc tgtctgtgga atgttg

36

<210> 37
<211> 39
<212> DNA
<213> Homo sapiens

<400> 37
gatcgatgac tatctctgac tctccgcgtg aacaggacg

39

<210> 38
<211> 39
<212> DNA
<213> Homo sapiens

<400> 38
gatccgtcct gttcacgcgg agagtcagag atagtcatc

39

<210> 39
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2

<400> 39
cggcatccgg ctgcccctgc gtagcggtct gggtggtgct ccactgggtc tgcgtctgcc 60
ccgggagacc gacgaag 77

<210> 40
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2

<400> 40
cttcgtcggt ctccccgggc agacgcagac ccagtggagc accaccaga ccgctacgca 60
ggggcagccg gatgcgg 77

<210> 41
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase 8
Cleavage Site

<400> 41
gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase 8
Cleavage Site

<400> 42
gatccgtcgg tttcgataacc agagtccagc ggagagtcag agatagtcac c 51

<210> 43
<211> 32
<212> DNA
<213> Homo sapiens

<400> 43
aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44
<211> 36
<212> DNA
<213> Homo sapiens

<400> 44
gaaagcttcc atgactcatc tgtctgtgga atgttg 36

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 45
gatcgcatca tcaccatcac catg 24

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 46
gatccatggat gatgggtatg atgc 24

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
gactgaccac tcgaccaggat tc 22

<210> 48
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
cgaattaaat tccagcacac tggctta 26

<210> 50
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 50
atggcccaag ccctgccctg gtcctgctg tggatggcg cgggagtgct gcctgccac 60
ggcacccagc acggcatccg gctgccctg cgcaagcgcc tggggggcgc cccctgggg 120
ctgcggctgc cccggagac cgacgaagag cccgaggagc cccggccggag gggcagcttt 180

gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgacagac gctcaacatc ctggggata caggcagcag taactttgca 300
gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtcacgaca 360
tacccgggacc tccggaaaggg tttgtatgtg ccctacaccc agggcaagt ggaaggggag 420
ctgggcaccc acctgtaag catccccat ggcggcaacg tcactgtgcg tgccaacatt 480
gctgcccata ctaaatcaga caagttcttc atcaacggct ccaactgggaa aggcatcctg 540
ggctggccct atgctgagat tgccaggctt ttgtgtgctg gcttccccc caaccagtct 600
gaagtgctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctgcgtgtac 660
acaggcagtc tctggatac acccatccgg cgggagtggt attatgaggt catcattgtg 720
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
agcattgtgg acagtggcac caccacccctt cggttgcacca agaaagtgtt tgaagctgca 840
gtcaaatcca tcaaggcagc ctccctccacg gagaagttcc ctgatggttt ctggctagga 900
gagcagctgg tttgtggca agcaggcacc accccttggaa acatttccc agtcatctca 960
ctctacctaa tgggtgaggt taccaaccag tccttccgc tcaccatctt tccgcagcaa 1020
tacctgccc cagtggaa tttgtggccacg tcccaagacg actgttacaa gtttgcac 1080
tcacagtcat ccacgggcac ttgttatggaa gctgttatca tggaggcctt ctacgttgac 1140
tttgatcggg cccgaaaacg aattggctt gctgtcagcg cttgccatgt gcacgatgag 1200
ttcaggacgg cagcgggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
aacattccac agacagatga gtcatga 1287

<210> 51
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 51
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425

<210> 52
<211> 1305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 52
atggcccaag ccctccccctg gctcctgctg tggatggcg cgggagtgct gcctgccccac 60
ggcacccagc acggcatccg gctccccctg cgcagcggcc tggggggcgc cccctgggg 120
ctgcggctgc cccggagac cgacgaagag cccgaggagc cccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240

gtgggcagcc ccccgccagac gctcaacatc ctggggata caggcagcag taactttgca 300
gtgggtgctg cccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tggatgtg ccctacaccc agggcaagt ggaaggggag 420
ctgggcaccc acctgtaag catccccat ggcccaacg tcactgtgcg tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg 540
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tcacagtcat ccacgggcac tgttatggaa gctgttatca tggaggcctt ctacgttg 1140
tttgatcg 1200
ttcaggacgg cagcggtgga aggcccttt gtcaccttgg acatggaaga ctgtggctac 1260
aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

<210> 53

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 53

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225 230 235 240

Arg Val Glu Ile Asn Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His
420 425 430

His His

<210> 54

<211> 2310

<212> DNA

<213> Homo sapiens

<400> 54

atgctgcccc gtttggcaact gtcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccaactgatg gtaatgctgg cctgctggct gaacccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180

acctgcattg ataccaagga aggcattcgt cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaacca ccagtgacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcacagc ccatccccac ttgtgattc cctaccgtg cttagttgg 360
gagtttggtaa gtgatgcct ttcgttct gacaagtgc aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtg ccaaagagac atgcagttag 480
aagagtagcca acttgcacatca ctacggcatg ttgctgcct gcggaattga caagttccga 540
ggggtagagt ttgtgttgc cccactggct gaagaaagtgc acaatgtgga ttctgctgat 600
gcccaggagg atgactcgga tgcgtgggg ggcggagcag acacagacta tgcatatggg 660
agtgaagaca aagtagtgc aatgcacatgc gaggaaagaag tggctgagggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgtatggg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagagggtgt tcgagaggtg tgctctgaa ac aagccgagac gggccgtgc 900
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cctgttaaac ttccatacaac agcagccagt accctgtat ccgttgacaa gtatctcgag 1140
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aagcaccgag agagaatgtc ccaggatcatg agagaatggg aagaggcaga acgtcaagca 1260
aagaacttgc ctaaaactgtga taagaaggca gttatccagc atttccagga gaaagtggaa 1320
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gaacagaagg acagacagca caccctaaag catttcgagc atgtgcgcatttgcgat 1560
aagaaagccg ctcagatccg gtcccccaggat atgacacacc tccgtgtat ttatgagcgc 1620
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gcaatcattt gactcatggt gggcggttt gtcatacgca cagtgatcgatcatcaccttg 2160
gtgatgctga agaagaaaca gtacacatcc attcatcatg gtgtggggaa ggttgacgcc 2220
gtctgcaccc cagaggagcg ccacctgtcc aagatgcagc agaacggcta cgaaaatcca 2280
acctacaagt tcttgagca gatgcagaaac 2310

<210> 55

<211> 770

<212> PRT

<213> Homo sapiens

<400> 55

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Val Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 56
<211> 2253
<212> DNA
<213> Homo sapiens

<400> 56

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<210> 57

<211> 751
<212> PRT
<213> Homo sapiens

<400> 57

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg

1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro

20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln

35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
565 570 575

Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
 740 745 750

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<210> 58
<211> 2316
<212> DNA
<213> Homo sapiens
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<210> 59
<211> 772
<212> PRT
<213> *Homo sapiens*

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20

25

30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn Lys Lys
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<210> 60

<211> 2259

<212> DNA

<213> Homo sapiens

<400> 60

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cagatcacca atgtgttaga agccaaaccaa ccagtggacca tccagaactg gtgcaagcgg 300
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gcccgtgtca ccccaagagga gcccacccgtc tccaaatgc agcagaacgg ctacgaaaat 2220
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<210> 61
<211> 753
<212> PRT
<213> Homo sapiens

<400> 61
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20 25 30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
565 570 575

Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys
740 745 750

Lys

<210> 62

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 62

Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 63

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 63

Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5 10

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 64
Ser Glu Val Lys Met Asp Ala Glu Phe Arg
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<210> 65
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 65
Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg
1 5 10 15

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 66
Asn Leu Asp Ala
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<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 67
Glu Val Lys Met Asp Ala Glu Phe
1 5

<210> 68
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 68
Gly Arg Arg Gly Ser
1 5

<210> 69
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 69
Thr Gln His Gly Ile Arg
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 70

Glu Thr Asp Glu Glu Pro
1 5

<210> 71
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 71
Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro
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<210> 72
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 72

Asp Ala Glu Phe Arg
1 5

<210> 73
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 73

Ser Glu Val Asn Leu
1 5

<210> 74
<211> 4

<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Peptide

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<220>
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<220>
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<400> 74
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